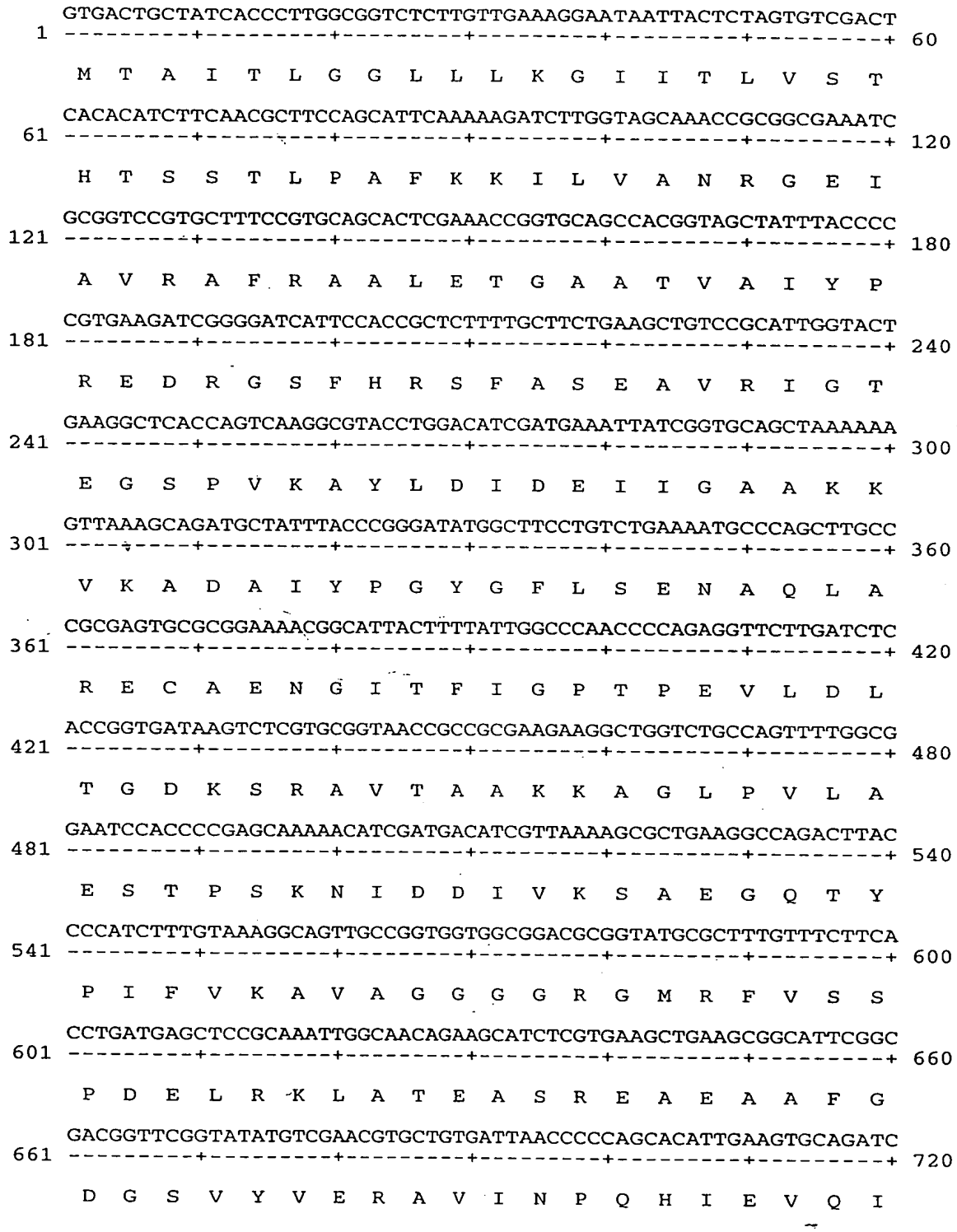

FIG. 1A

```
     CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT
 721 ---------+---------+---------+---------+---------+---------+ 780
      L  G  D  R  T  G  E  V  V  H  L  Y  E  R  D  C  S  L  Q  R

     CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT
 781 ---------+---------+---------+---------+---------+---------+ 840
      R  H  Q  K  V  V  E  I  A  P  A  Q  H  L  D  P  E  L  R  D

     CGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC
 841 ---------+---------+---------+---------+---------+---------+ 900
      R  I  C  A  D  A  V  K  F  C  R  S  I  G  Y  Q  G  A  G  T

     GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC
 901 ---------+---------+---------+---------+---------+---------+ 960
      V  E  F  L  V  D  E  K  G  N  H  V  F  I  E  M  N  P  R  I

     CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG
 961 ---------+---------+---------+---------+---------+---------+ 1020
      Q  V  E  H  T  V  T  E  E  V  T  E  V  D  L  V  K  A  Q  M

     CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC
1021 ---------+---------+---------+---------+---------+---------+ 1080
      R  L  A  A  G  A  T  L  K  E  L  G  L  T  Q  D  K  I  K  T

     CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA
1081 ---------+---------+---------+---------+---------+---------+ 1140
      H  G  A  A  L  Q  C  R  I  T  T  E  D  P  N  N  G  F  R  P

     GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200
      D  T  G  T  I  T  A  Y  R  S  P  G  G  A  G  V  R  L  D  G

     GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC
1201 ---------+---------+---------+---------+---------+---------+ 1260
      A  A  Q  L  G  G  E  I  T  A  H  F  D  S  M  L  V  K  M  T

     TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC
1261 ---------+---------+---------+---------+---------+---------+ 1320
      C  R  G  S  D  F  E  T  A  V  A  R  A  Q  R  A  L  A  E  F

     ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC
1321 ---------+---------+---------+---------+---------+---------+ 1380
      T  V  S  G  V  A  T  N  I  G  F  L  R  A  L  L  R  E  E  D

     TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT
1381 ---------+---------+---------+---------+---------+---------+ 1440
      F  T  S  K  R  I  A  T  G  F  I  G  D  H  P  H  L  L  Q  A
```

FIG. 1B

```
     CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500
      P  P  A  D  D  E  Q  G  R  I  L  D  Y  L  A  D  V  T  V  N

     AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC
1501 ---------+---------+---------+---------+---------+---------+ 1560
      K  P  H  G  V  R  P  K  D  V  A  A  P  I  D  K  L  P  N  I

     AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG
1561 ---------+---------+---------+---------+---------+---------+ 1620
      K  D  L  P  L  P  R  G  S  R  D  R  L  K  Q  L  G  P  A  A

     TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT
1621 ---------+---------+---------+---------+---------+---------+ 1680
      F  A  R  D  L  R  E  Q  D  A  L  A  V  T  D  T  T  F  R  D

     GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG
1681 ---------+---------+---------+---------+---------+---------+ 1740
      A  H  Q  S  L  L  A  T  R  V  R  S  F  A  L  K  P  A  A  E

     GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC
1741 ---------+---------+---------+---------+---------+---------+ 1800
      A  V  A  K  L  T  P  E  L  L  S  V  E  A  W  G  G  A  T  Y

     GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
      D  V  A  M  R  F  L  F  E  D  P  W  D  R  L  D  E  L  R  E

     GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC
1861 ---------+---------+---------+---------+---------+---------+ 1920
      A  M  P  N  V  N  I  Q  M  L  L  R  G  R  N  T  V  G  Y  T

     CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC
1921 ---------+---------+---------+---------+---------+---------+ 1980
      P  Y  P  D  S  V  C  R  A  F  V  K  E  A  A  S  S  G  V  D

     ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA
1981 ---------+---------+---------+---------+---------+---------+ 2040
      I  F  R  I  F  D  A  L  N  D  V  S  Q  M  R  P  A  I  D  A

     GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT
2041 ---------+---------+---------+---------+---------+---------+ 2100
      V  L  E  T  N  T  A  V  A  E  V  A  M  A  Y  S  G  D  L  S

     GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC
2101 ---------+---------+---------+---------+---------+---------+ 2160
      D  P  N  E  K  L  Y  T  L  D  Y  Y  L  K  M  A  E  E  I  V

     AAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG
2161 ---------+---------+---------+---------+---------+---------+ 2220
      K  S  G  A  H  I  L  A  I  K  D  M  A  G  L  L  R  P  A  A
```

FIG. 1C

```
      GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC
2221 ---------+---------+---------+---------+---------+---------+ 2280

       V  T  K  L  V  T  A  L  R  R  E  F  D  L  P  V  H  V  H  T

      CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT
2281 ---------+---------+---------+---------+---------+---------+ 2340

       H  D  T  A  G  G  Q  L  A  T  Y  F  A  A  A  Q  A  G  A  D

      GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC
2341 ---------+---------+---------+---------+---------+---------+ 2400

       A  V  D  G  A  S  A  P  L  S  G  T  T  S  Q  P  S  L  S  A

      ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT
2401 ---------+---------+---------+---------+---------+---------+ 2460

       I  V  A  A  F  A  H  T  R  R  D  T  G  L  S  L  E  A  V  S

      GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC
2461 ---------+---------+---------+---------+---------+---------+ 2520

       D  L  E  P  Y  W  E  A  V  R  G  L  Y  L  P  F  E  S  G  T

      CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG
2521 ---------+---------+---------+---------+---------+---------+ 2580

       P  G  P  T  G  R  V  Y  R  H  E  I  P  G  G  Q  L  S  N  L

      CGTGCACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACTAC
2581 ---------+---------+---------+---------+---------+---------+ 2640

       R  A  Q  A  T  A  L  G  L  A  D  R  F  E  L  I  E  D  N  Y

      GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT
2641 ---------+---------+---------+---------+---------+---------+ 2700

       A  A  V  N  E  M  L  G  R  P  T  K  V  T  P  S  S  K  V  V

      GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC
2701 ---------+---------+---------+---------+---------+---------+ 2760

       G  D  L  A  L  H  L  V  G  A  G  V  D  P  A  D  F  A  A  D

      CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC
2761 ---------+---------+---------+---------+---------+---------+ 2820

       P  Q  K  Y  D  I  P  D  S  V  I  A  F  L  R  G  E  L  G  N

      CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC
2821 ---------+---------+---------+---------+---------+---------+ 2880

       P  P  G  G  W  P  E  P  L  R  T  R  A  L  E  G  R  S  E  G

      AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC
2881 ---------+---------+---------+---------+---------+---------+ 2940

       K  A  P  L  T  E  V  P  E  E  E  Q  A  H  L  D  A  D  D  S
```

FIG. 1D

```
                AAGGAACGTCGCAACAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC
2941 ---------+---------+---------+---------+---------+---------+---------+ 3000

                 K   E   R   R   N   S   L   N   R   L   L   F   P   K   P   T   E   E   F   L

                GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA
3001 ---------+---------+---------+---------+---------+---------+---------+ 3060

                 E   H   R   R   R   F   G   N   T   S   A   L   D   D   R   E   F   F   Y   G

                CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT
3061 ---------+---------+---------+---------+---------+---------+---------+ 3120

                 L   V   E   G   R   E   T   L   I   R   L   P   D   V   R   T   P   L   L   V

                CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC
3121 ---------+---------+---------+---------+---------+---------+---------+ 3180

                 R   L   D   A   I   S   E   P   D   D   K   G   M   R   N   V   V   A   N   V

                AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC
3181 ---------+---------+---------+---------+---------+---------+---------+ 3240

                 N   G   Q   I   R   P   M   R   V   R   D   R   S   V   E   S   V   T   A   T

                GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC
3241 ---------+---------+---------+---------+---------+---------+---------+ 3300

                 A   E   K   A   D   S   S   N   K   G   H   V   A   A   P   F   A   G   V   V

                ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG
3301 ---------+---------+---------+---------+---------+---------+---------+ 3360

                 T   V   T   V   A   E   G   D   E   V   K   A   G   D   A   V   A   I   I   E

                GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG
3361 ---------+---------+---------+---------+---------+---------+---------+ 3420

                 A   M   K   M   E   A   T   I   T   A   S   V   D   G   K   I   E   R   V   V

                GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA
3421 ---------+---------+---------+---------+---------+---------+---- 3474

                 V   P   A   A   T   K   V   E   G   G   D   L   I   V   V   V   S   *
```

FIG. 1E

```
                                1
ATCC 21253   pyc                                  MST  HTSSTLPAFK  KILVANRGEI  AVRAFRAALE  50
NRRL B-11474 pyc                MTAITLGGLL  LKGIITLV

                                51
ATCC 21253   pyc                                                                           100
NRRL B-11474 pyc                TGAATVAIYP  REDRGSFHRS  FASEAVRIGT  EGSPVKAYLD  IDEIIGAAKK

                                101
ATCC 21253   pyc                                                                           150
NRRL B-11474 pyc                VKADAIYPGY  GFLSENAQLA  RECAENGITF  IGPTPEVLDL  TGDKSRAVTA

                                151
ATCC 21253   pyc                                                                           200
NRRL B-11474 pyc                AKKAGLPVLA  ESTPSKNIDE  IVKSAEGQTY  PIFVKAVAGG  GGRGMRFVAS
                                                     D                                   S

                                201
ATCC 21253   pyc                                                                           250
NRRL B-11474 pyc                PDELRKLATE  ASREAEAAFG  DGAVYVERAV  INPQHIEVQI  LGDHTGEVVH
                                                          S                            R

                                251
ATCC 21253   pyc                                                                           300
NRRL B-11474 pyc                LYERDCSLQR  RHQKVVEIAP  AQHLDPELRD  RICADAVKFC  RSIGYQGAGT

                                301
ATCC 21253   pyc                                                                           350
NRRL B-11474 pyc                VEFLVDEKGN  HVFIEMNPRI  QVEHTVTEEV  TEVDLVKAQM  RLAAGATLKE

                                351
ATCC 21253   pyc                                                                           400
NRRL B-11474 pyc                LGLTQDKIKT  HGAALQCRIT  TEDPNNGFRP  DTGTITAYRS  PGGAGVRLDG

                                401
ATCC 21253   pyc                                                                           450
NRRL B-11474 pyc                AAQLGGEITA  HFDSMLVKMT  CRGSDFETAV  ARAQRALAEF  TVSGVATNIG

                                451
ATCC 21253   pyc                                                                           500
NRRL B-11474 pyc                FLRALLREED  FTSKRIATGF  IADHPHLLQA  PPADDEQGRI  LDYLADVTVN
                                                         G

                                501
ATCC 21253   pyc                                                                           550
NRRL B-11474 pyc                KPHGVRPKDV  AAPIDKLPNI  KDLPLPRGSR  DRLKQLGPAA  FARDLREQDA

                                551
ATCC 21253   pyc                                                                           600
NRRL B-11474 pyc                LAVTDTTFRD  AHQSLLATRV  RSFALKPAAE  AVAKLTPELL  SVEAWGGATY

                                601
ATCC 21253   pyc                                                                           650
NRRL B-11474 pyc                DVAMRFLFED  PWDRLDELRE  AMPNVNIQML  LRGRNTVGYT  PYPDSVCRAF

                                651
ATCC 21253   pyc                                                                           700
NRRL B-11474 pyc                VKEAASSGVD  IFRIFDALND  VSQMRPAIDA  VLETNTAVAE  VAMAYSGDLS

                                701
ATCC 21253   pyc                                                                           750
NRRL B-11474 pyc                DPNEKLYTLD  YYLKMAEEIV  KSGAHILAIK  DMAGLLRPAA  VTKLVTALRR

                                751
ATCC 21253   pyc                                                                           800
NRRL B-11474 pyc                EFDLPVHVHT  HDTAGGQLAT  YFAAAQAGAD  AVDGASAPLS  GTTSQPSLSA
```

FIG. 2A

Strain	Gene	Sequence
		801 ... 850
ATCC 21253	pyc	IVAAFAHTRR DTGLSLEAVS DLEPYWEAVR GLYLPFESGT PGPTGRVYRH
NRRL B-11474	pyc	
		851 ... 900
ATCC 21253	pyc	EIPGGQLSNL RAQATALGLA DRFELIEDNY AAVNEMLGRP TKVTPSSKVV
NRRL B-11474	pyc	
		901 ... 950
ATCC 21253	pyc	GDLALHLVGA GVDPADFAAD PQKYDIPDSV IAFLRGELGN PPGGWPEPLR
NRRL B-11474	pyc	
		951 ... 1000
ATCC 21253	pyc	TRALEGRSEG KAPLTEVPEE EQAHLDADDS KERRNSLNRL LFPKPTEEFL
NRRL B-11474	pyc	
		1001 ... 1050
ATCC 21253	pyc	EHRRRFGNTS ALDDREFFYG LVEGRETLIR LPDVRTPLLV RLDAISEPDD
NRRL B-11474	pyc	
		1051 ... 1100
ATCC 21253	pyc	KGMRNVVANV NGQIRPMRVR DRSVESVTAT AEKADSSNKG HVAAPFAGVV
NRRL B-11474	pyc	
		1101 ... 1150
ATCC 21253	pyc	TVTVAEGDEV KAGDAVAIIE AMKMEATITA SVDGKIDRVV VPAATKVEGG
NRRL B-11474	pyc	E (under position 1133)
		1151
ATCC 21253	pyc	DLIVVVS
NRRL B-11474	pyc	

FIG. 2B

GTGACTGCTATCACCCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCGACT
CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC
GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC
CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACT
GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA
GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCTGTCTGAAAATGCCCAGCTTGCC
CGCGAGTGCGCGGAAAACGGCATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTC
ACCGGTGATAAGTCTCGTGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCG
GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC
CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA
CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCGGC
GACGGTTCGGTATATGTCGAACGTGCTGTGATTAACCCCCAGCACATTGAAGTGCAGATC
CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT
CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT
CGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC
GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC
CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG
CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC
CACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCGCCCA
GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGT
GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC
TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGCGCGCGTTGGCTGAGTTC
ACCGTGTCTGGTGTTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC
TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT
CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC
AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC
AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG
TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT
GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG
GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC
GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG
GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC
CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC
ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA
GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT
GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC
AAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG
GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC
CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT
GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC
ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT
GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC
CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG
CGTGCACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACTAC
GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT
GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC
CCACAAAAGTACGACATCCCAGACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC
CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC
AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC
AAGGAACGTCGCAACAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC
GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA
CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT
CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC
AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC
GCAGAAAAGGCAGATTCCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTC
ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG
GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG
GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA

FIG. 3A

MTAITLGGLLLKGIITLVSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYP
REDRGSFHRSFASEAVRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLA
RECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTY
PIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQI
LGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGT
VEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKT
HGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMT
CRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQA
PPADDEQGRILDYLADVTVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAA
FARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATY
DVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVD
IFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIV
KSGAHILAIKDMAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGAD
AVDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGT
PGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVV
GDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEG
KAPLTEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYG
LVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTAT
AEKADSSNKGHVAAPFAGVVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVV
VPAATKVEGGDLIVVVS

FIG. 3B

Effect of various substrate concentrations on pyruvate carboxylase activity from *C. glutamicum* BF100 (○) and ATCC 21253 (●).

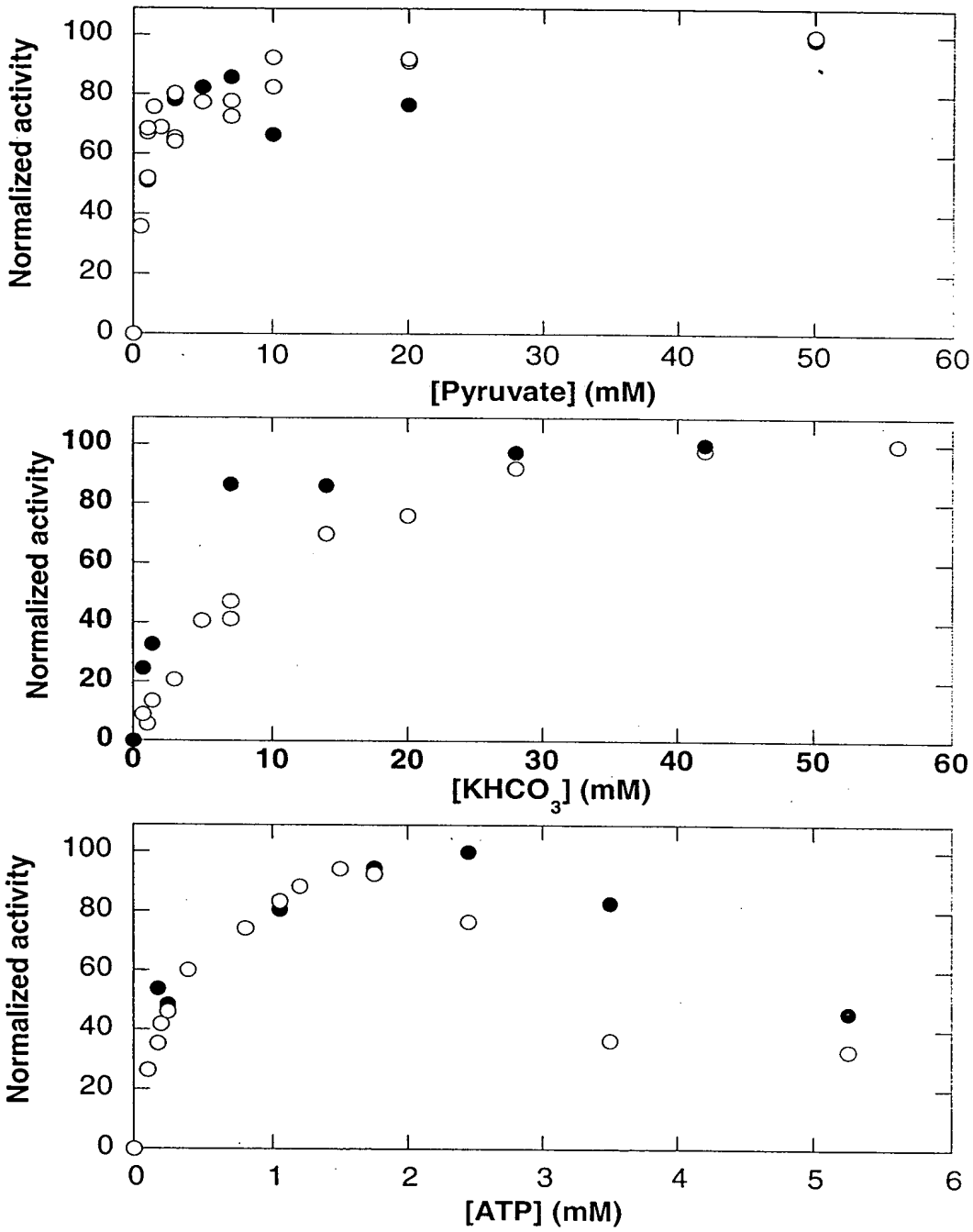

FIG. 4

Effect of aspartate on the activity of pyruvate carboxylase from *C. glutamicum* BF100 (○) and ATCC 21253 ( ).

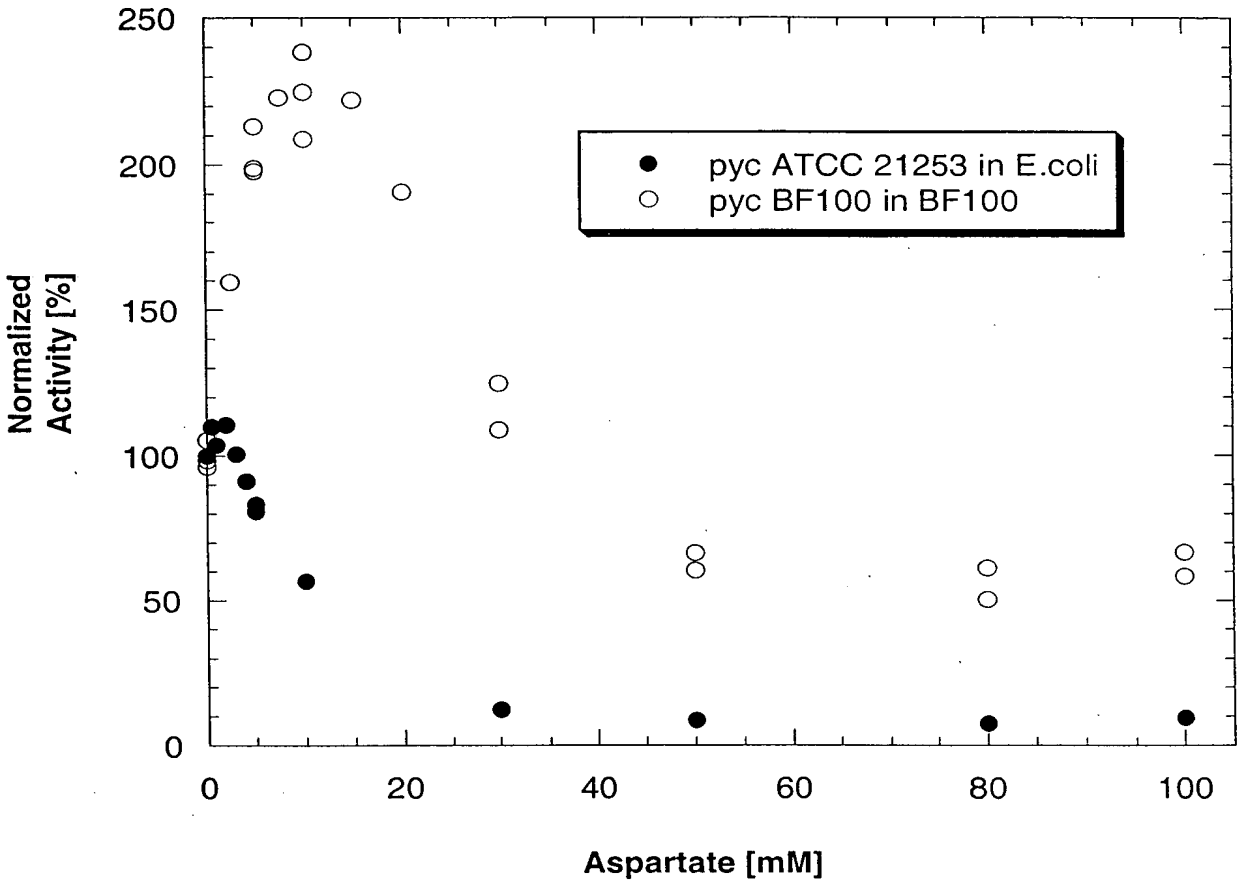

FIG. 5

Effect of Acetyl-CoA on pyruvate carboxylase activity from *C. glutamicum* BF100 (O) and ATCC 21253 ( ).

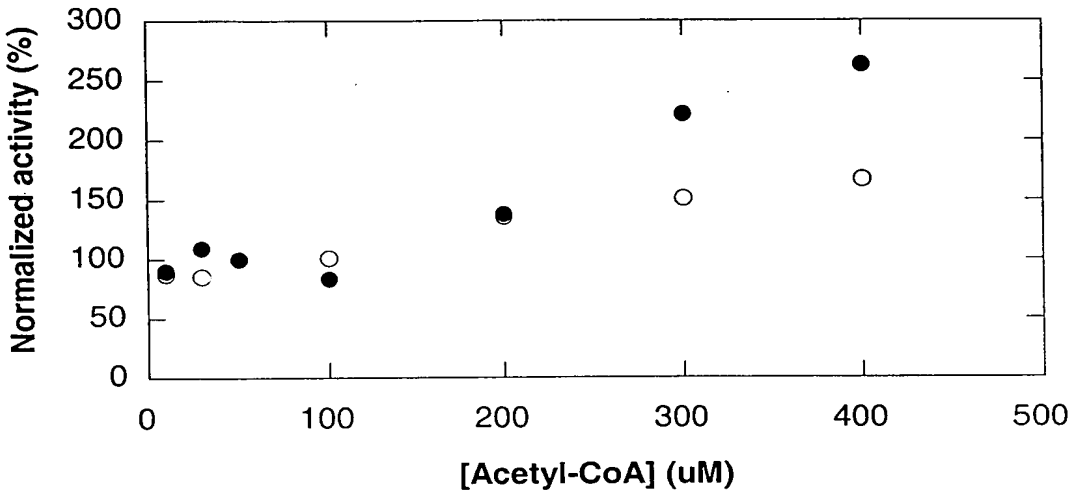

FIG. 6